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SEQUENCE LISTING

<110> Takeda Chemical Industries, Ltd.

<120> Novel Screening Method

<130> P04-117PCT

<150> JP 2002-093045

<151> 2002-03-28

<150> JP 2002-361580

<151> 2002-12-13

<160> 10

<170> PatentIn version 3.1

<210> 1

<211> 957

<212> DNA

<213> Rattus sp.

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<221> CDS

<222> (1)..(957)

<223> rat-derived rCB7T084

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ccc acc atg gac cct gtg acc tgg gtt tac ttt tca gtg aca ttc ctg	96
Pro Thr Met Asp Pro Val Thr Trp Val Tyr Phe Ser Val Thr Phe Leu	
20 25 30	
gcc atg gcc acc tgt gtg tgt ggg ata gtg ggc aac tcc atg gtg att	144
Ala Met Ala Thr Cys Val Cys Gly Ile Val Gly Asn Ser Met Val Ile	
35 40 45	
tgg cta ctg agt ttc cac agt gtg cag agg tcc ccc ttc tgc acc tac	192
Trp Leu Leu Ser Phe His Ser Val Gln Arg Ser Pro Phe Cys Thr Tyr	
50 55 60	
gtg ctc aac ctg gcg gtg gcc gac ctc ctc ttc ctg ctc tgc atg gcc	240
Val Leu Asn Leu Ala Val Ala Asp Leu Leu Phe Leu Leu Cys Met Ala	
65 70 75 80	
tcc ctg ctc agt ctg gaa aca ggg ccc ctg ctc aca gcc agc acc tcc	288
Ser Leu Leu Ser Leu Glu Thr Gly Pro Leu Leu Thr Ala Ser Thr Ser	
85 90 95	
gcc aga gtc tac gag ggg atg aag aga atc aag tac ttt gcc tac aca	336
Ala Arg Val Tyr Glu Gly Met Lys Arg Ile Lys Tyr Phe Ala Tyr Thr	
100 105 110	
gca ggc ctg agc ctg ctg acg gcc atc agc acc cag cgc tgt ctc tcc	384
Ala Gly Leu Ser Leu Leu Thr Ala Ile Ser Thr Gln Arg Cys Leu Ser	
115 120 125	
gtg ctt ttc ccc atc tgg tat aag tgc cac cgg ccc cag cac ctg tcg	432
Val Leu Phe Pro Ile Trp Tyr Lys Cys His Arg Pro Gln His Leu Ser	
130 135 140	
ggg gtg gta tgt ggt gtg ctg tgg gca ctg gcc ctc ctg atg aac ttc	480

Gly	Val	Val	Cys	Gly	Val	Leu	Trp	Ala	Leu	Ala	Leu	Leu	Met	Asn	Phe		
145					150					155					160		
ctg	gct	tct	ttc	ttc	tgt	gtt	caa	ttc	tgg	cat	ccc	gac	aaa	tac	cag	528	
Leu	Ala	Ser	Phe	Phe	Cys	Val	Gln	Phe	Trp	His	Pro	Asp	Lys	Tyr	Gln		
				165					170						175		
tgc	ttc	aag	gtg	gac	atg	gtt	ttc	aac	agt	ctt	atc	ctg	ggg	atc	ttc	576	
Cys	Phe	Lys	Val	Asp	Met	Val	Phe	Asn	Ser	Leu	Ile	Leu	Gly	Ile	Phe		
			180					185					190				
atg	ccc	gtc	atg	gtc	ctg	acc	agc	gcc	atc	atc	ttc	atc	cgc	atg	cga	624	
Met	Pro	Val	Met	Val	Leu	Thr	Ser	Ala	Ile	Ile	Phe	Ile	Arg	Met	Arg		
			195					200					205				
aag	aac	agc	ctg	ctg	cag	aga	cgg	cag	cct	cgg	cgg	ctc	tac	gtg	gtc	672	
Lys	Asn	Ser	Leu	Leu	Gln	Arg	Arg	Gln	Pro	Arg	Arg	Leu	Tyr	Val	Val		
	210					215					220						
atc	ctg	act	tcc	gtc	ctt	gtc	ttc	ctt	acc	tgt	tct	ctg	ccg	ttg	ggc	720	
Ile	Leu	Thr	Ser	Val	Leu	Val	Phe	Leu	Thr	Cys	Ser	Leu	Pro	Leu	Gly		
	225				230					235					240		
atc	aac	tgg	ttc	tta	ctc	tac	tgg	gtg	gaa	ctg	ccg	cag	gcc	gtg	agg	768	
Ile	Asn	Trp	Phe	Leu	Leu	Tyr	Trp	Val	Glu	Leu	Pro	Gln	Ala	Val	Arg		
				245					250					255			
ctc	ctg	tac	gtc	tgc	tca	tca	cgc	ttc	tcc	tcg	tct	ttg	agc	agc	agc	816	
Leu	Leu	Tyr	Val	Cys	Ser	Ser	Arg	Phe	Ser	Ser	Ser	Leu	Ser	Ser	Ser		
			260					265					270				
gcc	aac	cca	gtc	atc	tac	ttc	ctc	gtg	ggc	agc	cag	aag	agc	cac	cgg	864	
Ala	Asn	Pro	Val	Ile	Tyr	Phe	Leu	Val	Gly	Ser	Gln	Lys	Ser	His	Arg		
		275					280					285					
ctg	cag	gag	tct	ctg	ggg	gct	gtg	ctg	ggg	cgg	gca	ctt	cag	gac	gag	912	
Leu	Gln	Glu	Ser	Leu	Gly	Ala	Val	Leu	Gly	Arg	Ala	Leu	Gln	Asp	Glu		
	290					295					300						
cct	gaa	ggc	agg	gag	acg	cca	tcc	aca	tgt	act	aat	gat	ggg	gtc		957	
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			20					25					30				
Ala	Met	Ala	Thr	Cys	Val	Cys	Gly	Ile	Val	Gly	Asn	Ser	Met	Val	Ile		
		35					40					45					
Trp	Leu	Leu	Ser	Phe	His	Ser	Val	Gln	Arg	Ser	Pro	Phe	Cys	Thr	Tyr		
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Val	Leu	Asn	Leu	Ala	Val	Ala	Asp	Leu	Leu	Phe	Leu	Leu	Cys	Met	Ala		
	65				70					75				80			
Ser	Leu	Leu	Ser	Leu	Glu	Thr	Gly	Pro	Leu	Leu	Thr	Ala	Ser	Thr	Ser		
			85					90					95				
Ala	Arg	Val	Tyr	Glu	Gly	Met	Lys	Arg	Ile	Lys	Tyr	Phe	Ala	Tyr	Thr		
		100						105					110				
Ala	Gly	Leu	Ser	Leu	Leu	Thr	Ala	Ile	Ser	Thr	Gln	Arg	Cys	Leu	Ser		
	115					120						125					
Val	Leu	Phe	Pro	Ile	Trp	Tyr	Lys	Cys	His	Arg	Pro	Gln	His	Leu	Ser		
	130					135						140					

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 145 150 155 160
 Leu Ala Ser Phe Phe Cys Val Gln Phe Trp His Pro Asp Lys Tyr Gln
 165 170 175
 Cys Phe Lys Val Asp Met Val Phe Asn Ser Leu Ile Leu Gly Ile Phe
 180 185 190
 Met Pro Val Met Val Leu Thr Ser Ala Ile Ile Phe Ile Arg Met Arg
 195 200 205
 Lys Asn Ser Leu Leu Gln Arg Arg Gln Pro Arg Arg Leu Tyr Val Val
 210 215 220
 Ile Leu Thr Ser Val Leu Val Phe Leu Thr Cys Ser Leu Pro Leu Gly
 225 230 235 240
 Ile Asn Trp Phe Leu Leu Tyr Trp Val Glu Leu Pro Gln Ala Val Arg
 245 250 255
 Leu Leu Tyr Val Cys Ser Ser Arg Phe Ser Ser Ser Leu Ser Ser Ser
 260 265 270
 Ala Asn Pro Val Ile Tyr Phe Leu Val Gly Ser Gln Lys Ser His Arg
 275 280 285
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 290 295 300
 Pro Glu Gly Arg Glu Thr Pro Ser Thr Cys Thr Asn Asp Gly Val
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 <221> CDS
 <222> (1)..(963)
 <223> human-derived TGR7

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 tat tcc aga ggg agc aca gtg cac acg gcc tac ctg gtg ctg agc tcc 96
 Tyr Ser Arg Gly Ser Thr Val His Thr Ala Tyr Leu Val Leu Ser Ser
 20 25 30
 ctg gcc atg ttc acc tgc ctg tgc ggg atg gca ggc aac agc atg gtg 144
 Leu Ala Met Phe Thr Cys Leu Cys Gly Met Ala Gly Asn Ser Met Val
 35 40 45
 atc tgg ctg ctg ggc ttt cga atg cac agg aac ccc ttc tgc atc tat 192
 Ile Trp Leu Leu Gly Phe Arg Met His Arg Asn Pro Phe Cys Ile Tyr
 50 55 60
 atc ctc aac ctg gcg gca gcc gac ctc ctc ttc ctc ttc agc atg gct 240
 Ile Leu Asn Leu Ala Ala Ala Asp Leu Leu Phe Leu Phe Ser Met Ala
 65 70 75 80
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 Ser Thr Leu Ser Leu Glu Thr Gln Pro Leu Val Asn Thr Thr Asp Lys
 85 90 95
 gtc cac gag ctg atg aag aga ctg atg tac ttt gcc tac aca gtg ggc 336
 Val His Glu Leu Met Lys Arg Leu Met Tyr Phe Ala Tyr Thr Val Gly
 100 105 110
 ctg agc ctg ctg acg gcc atc agc acc cag cgc tgt ctc tct gtc ctc 384
 Leu Ser Leu Leu Thr Ala Ile Ser Thr Gln Arg Cys Leu Ser Val Leu

115	120	125	
ttc cct atc tgg ttc aag tgt cac cgg ccc agg cac ctg tca gcc tgg			432
Phe Pro Ile Trp Phe Lys Cys His Arg Pro Arg His Leu Ser Ala Trp			
130	135	140	
gtg tgt ggc ctg ctg tgg acg ctc tgt ctc ctg atg aac ggg ttg acc			480
Val Cys Gly Leu Leu Trp Thr Leu Cys Leu Leu Met Asn Gly Leu Thr			
145	150	155	160
tct tcc ttc tgc agc aag ttc ttg aaa ttc aat gaa gat cgg tgc ttc			528
Ser Ser Phe Cys Ser Lys Phe Leu Lys Phe Asn Glu Asp Arg Cys Phe			
165	170	175	
agg gtg gac atg gtc cag gcc gcc ctc atc atg ggg gtc tta acc cca			576
Arg Val Asp Met Val Gln Ala Ala Leu Ile Met Gly Val Leu Thr Pro			
180	185	190	
gtg atg act ctg tcc agc ctg acc ctc ttt gtc tgg gtg cgg agg agc			624
Val Met Thr Leu Ser Ser Leu Thr Leu Phe Val Trp Val Arg Arg Ser			
195	200	205	
tcc cag cag tgg cgg cgg cag ccc aca cgg ctg ttc gtg gtg gtc ctg			672
Ser Gln Gln Trp Arg Arg Gln Pro Thr Arg Leu Phe Val Val Val Leu			
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gcc tct gtc ctg gtg ttc ctc atc tgt tcc ctg cct ctg agc atc tac			720
Ala Ser Val Leu Val Phe Leu Ile Cys Ser Leu Pro Leu Ser Ile Tyr			
225	230	235	240
tgg ttt gtg ctc tac tgg ttg agc ctg ccg ccc gag atg cag gtc ctg			768
Trp Phe Val Leu Tyr Trp Leu Ser Leu Pro Pro Glu Met Gln Val Leu			
245	250	255	
tgc ttc agc ttg tca cgc ctc tcc tcg tcc gta agc agc agc gcc aac			816
Cys Phe Ser Leu Ser Arg Leu Ser Ser Ser Val Ser Ser Ser Ala Asn			
260	265	270	
ccc gtc atc tac ttc ctg gtg ggc agc cgg agg agc cac agg ctg ccc			864
Pro Val Ile Tyr Phe Leu Val Gly Ser Arg Arg Ser His Arg Leu Pro			
275	280	285	
acc agg tcc ctg ggg act gtg ctc caa cag gcg ctt cgc gag gag ccc			912
Thr Arg Ser Leu Gly Thr Val Leu Gln Gln Ala Leu Arg Glu Glu Pro			
290	295	300	
gag ctg gaa ggt ggg gag acg ccc acc gtg ggc acc aat gag atg ggg			960
Glu Leu Glu Gly Gly Glu Thr Pro Thr Val Gly Thr Asn Glu Met Gly			
305	310	315	320
gct			963
Ala			

<210> 4
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 <212> PRT
 <213> Homo sapiens

<400> 4
 Met Asn Gln Thr Leu Asn Ser Ser Gly Thr Val Glu Ser Ala Leu Asn
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 Tyr Ser Arg Gly Ser Thr Val His Thr Ala Tyr Leu Val Leu Ser Ser
 20 25 30
 Leu Ala Met Phe Thr Cys Leu Cys Gly Met Ala Gly Asn Ser Met Val
 35 40 45
 Ile Trp Leu Leu Gly Phe Arg Met His Arg Asn Pro Phe Cys Ile Tyr
 50 55 60
 Ile Leu Asn Leu Ala Ala Ala Asp Leu Leu Phe Leu Phe Ser Met Ala
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 Ser Thr Leu Ser Leu Glu Thr Gln Pro Leu Val Asn Thr Thr Asp Lys

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<223> Probe, labeled 5'-terminal with FAM and 3'-terminal with TAMRA

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<212> DNA

<213> Artificial Sequence

<220>

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<400> 8

tgatgaactt cctggcttct ttc 23

<210> 9

<211> 22

<212> DNA

<213> Artificial Sequence

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<400> 9

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<210> 10

<211> 27

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